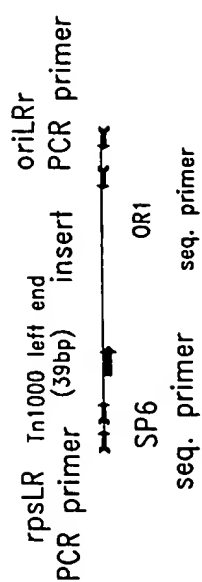
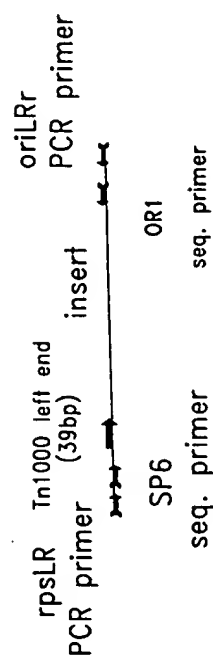
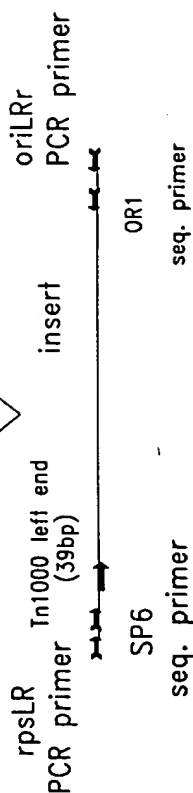
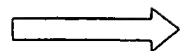


**FIG. 1**



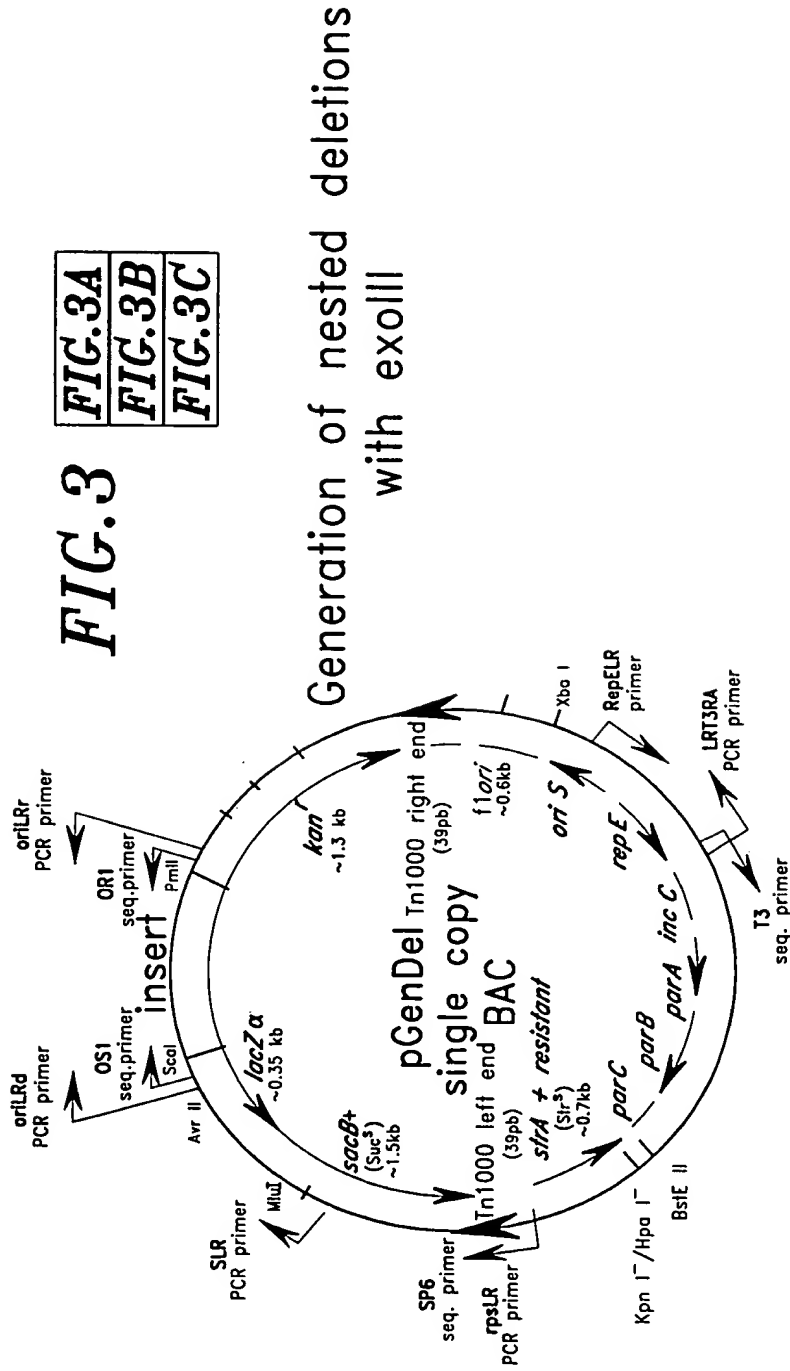


generation of templates  
by LR PCR  
from colonies



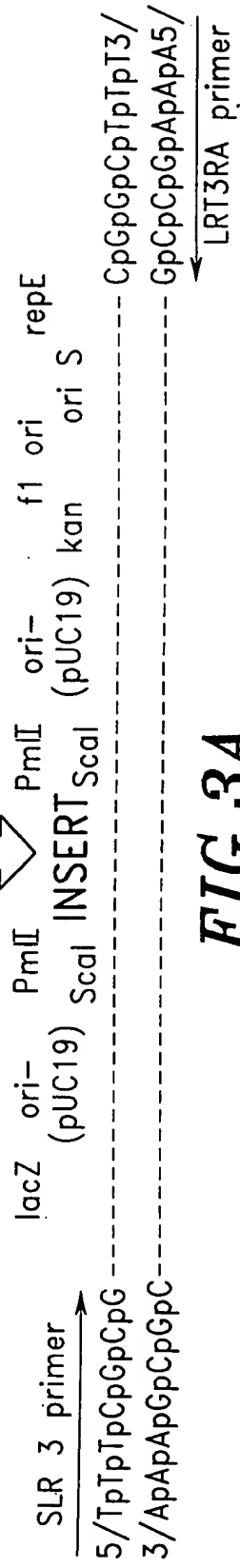
1. Forced cloning of blunt ended fragments into pGenDel by contra-selection on streptomycine plus kanaycine
2. Selection of intra transposed clones by plating on sucrose/kanamycine/Xgal media
3. Generation of templates by PCR from colonies.
4. Minimal tiling path determination by sizing

FIG.2C



kanamycine resistant, streptomycine resistant if introduced into streptomycine resistant cells, sucrose sensitive, faint blue on IPTG/Xgal plates

generation of linear substrates by LR PCR with SLR3 and LRT3RA primers from cells



**FIG. 3A**

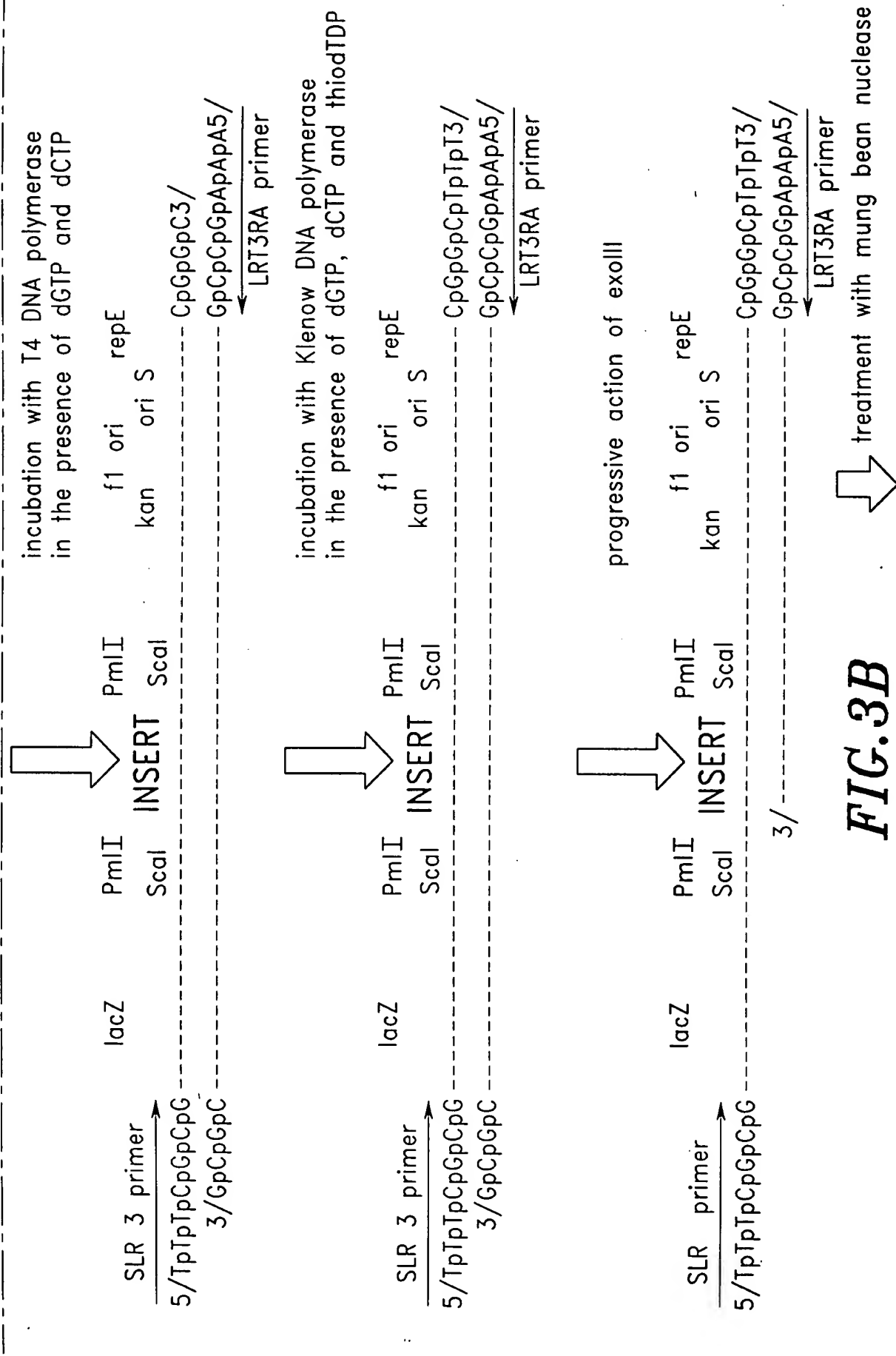
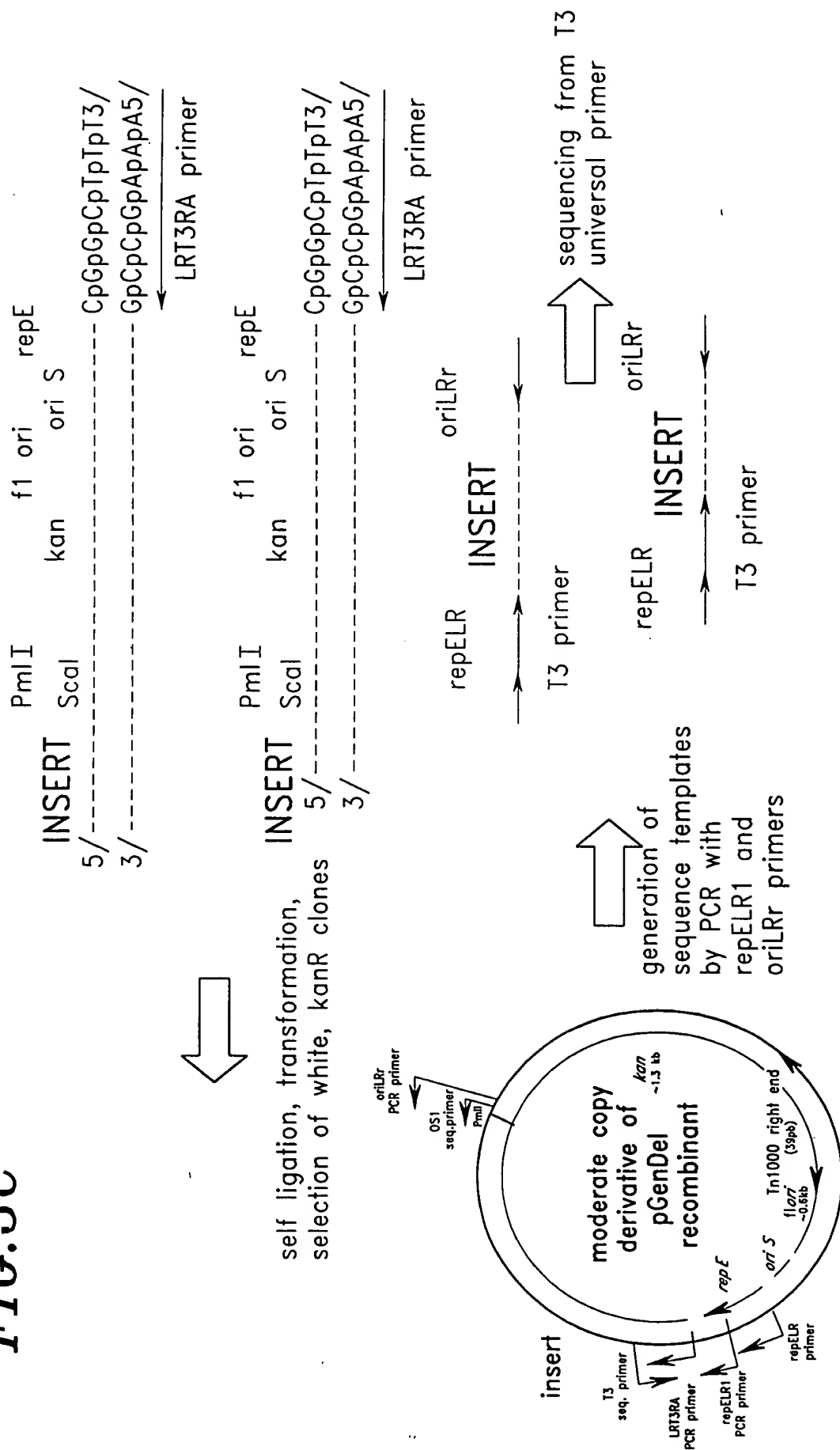
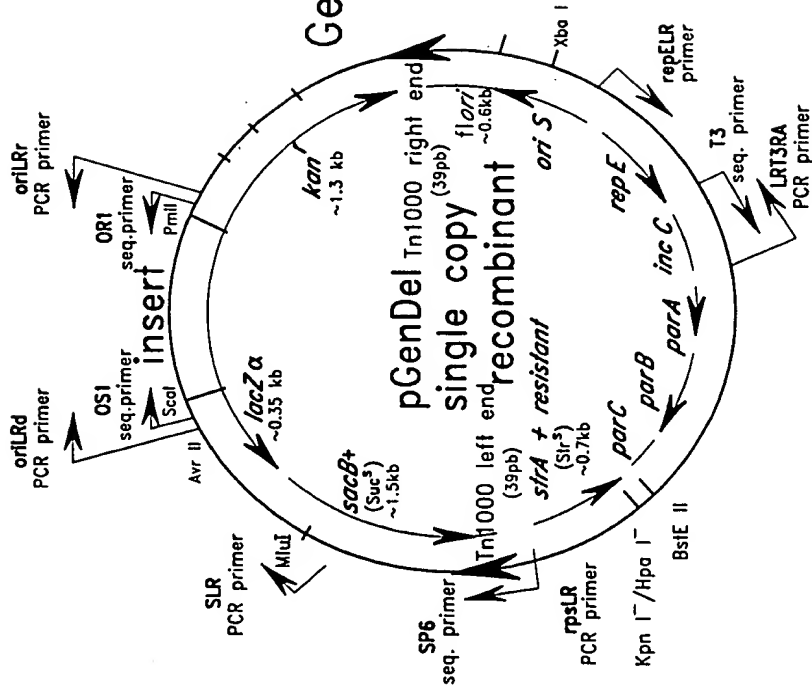


FIG. 3C



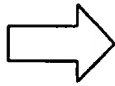
kanamycine resistant, streptomycine resistant if introduced into streptomycine resistant cells, sucrose sensitive, white on IPTG/Xgal plates



**FIG. 4**  
**FIG. 4A**  
**FIG. 4B**  
**FIG. 4C**

Generation of nested deletions  
 with Mung bean nuclease

kanamycine resistant, streptomycine resistant if introduced into streptomycine  
 resistant cells, sucrose sensitive, faint blue on IPTG/Xgal plates



generation of linear substrates by LR PCR  
 with SLR3 and LRT3RA primers from cells

5/TpTpTpCpGpCpG ----- CpGpGpCpTpTpT3/  
 3/ApApApGpCpGpC ----- GpCpGpCpApApA5/  
 SLR 3 primer → lacZ ori- PmlI ori- f1 ori repE  
 (pUC19) ScaI INSERT<sub>ScaI</sub> (pUC19) kan ori S ← LRT3RA primer

**FIG. 4A**

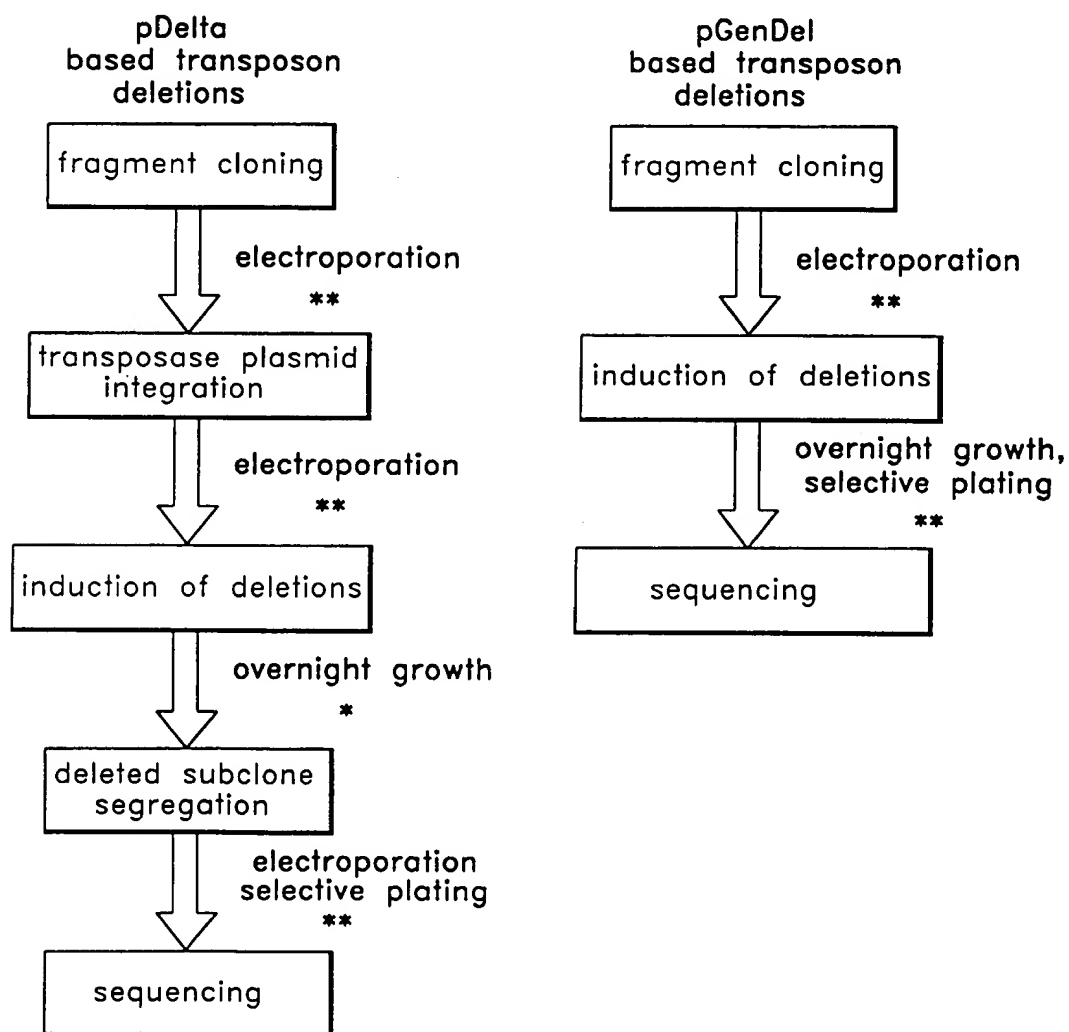






# FIG.5 FIG.5A FIG.5B

Comparison of different methods of  
nested deletion sequencing



\*shown in

\*- easy stages

\*\* - difficult stages

\*\*\* - very difficult stages

## FIG.5A

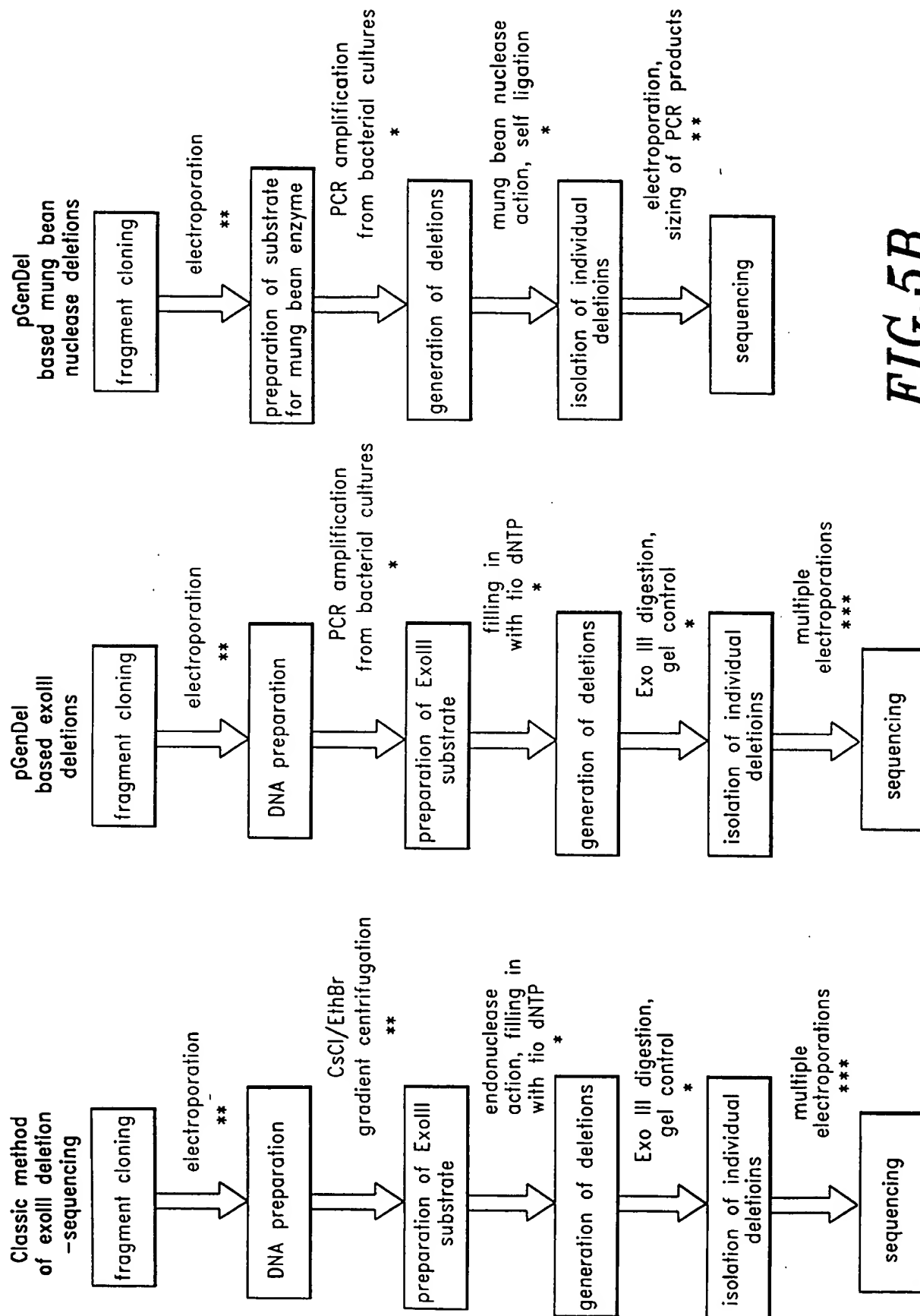
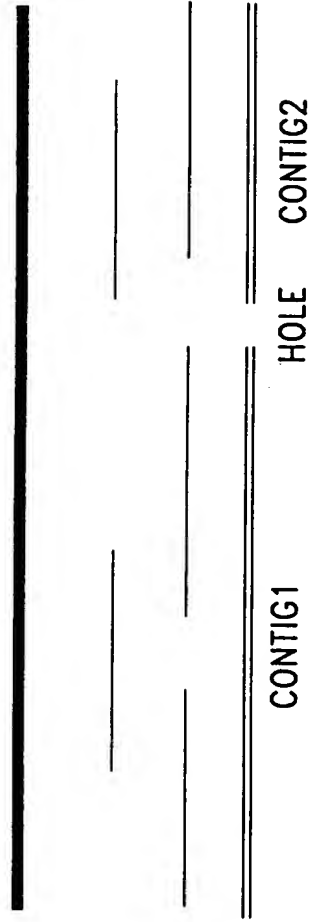


FIG. 5B

# THE SHOTGUN STRATEGY

INSERT

SEQUENCES



**FIG. 6**

# THE PAIRWISE STRATEGY

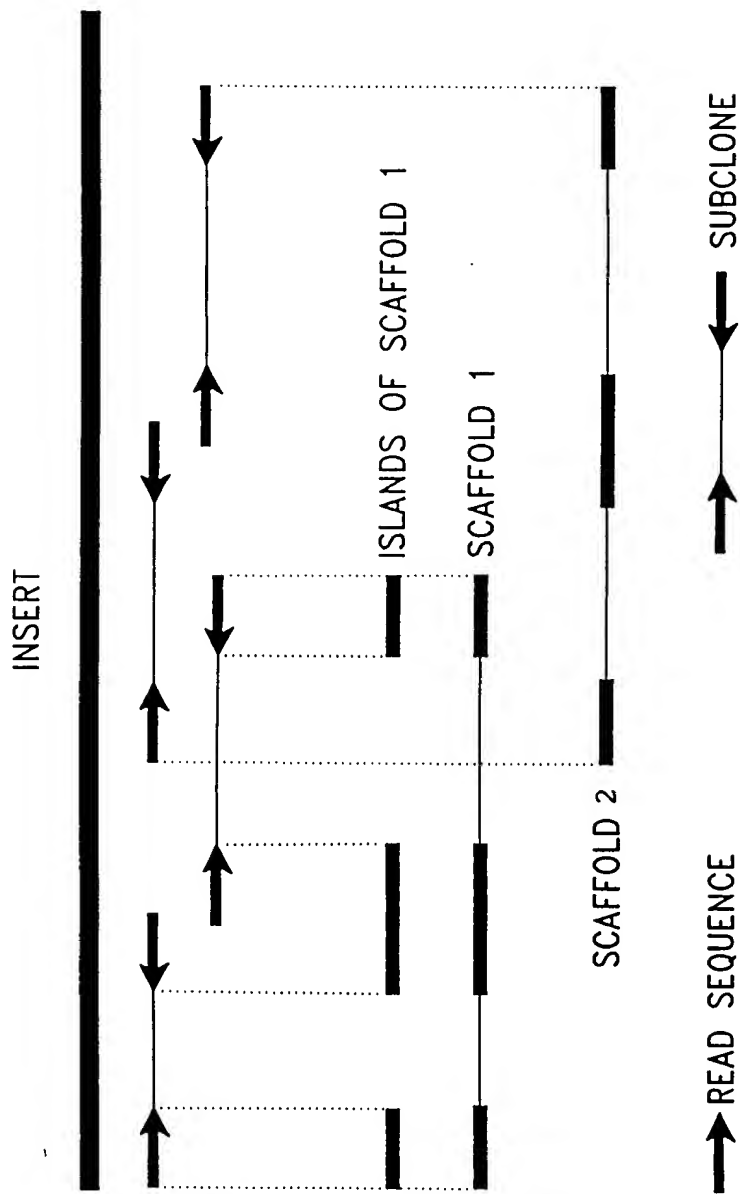


FIG. 7

# MULTIPLE NUCLEATION POINT

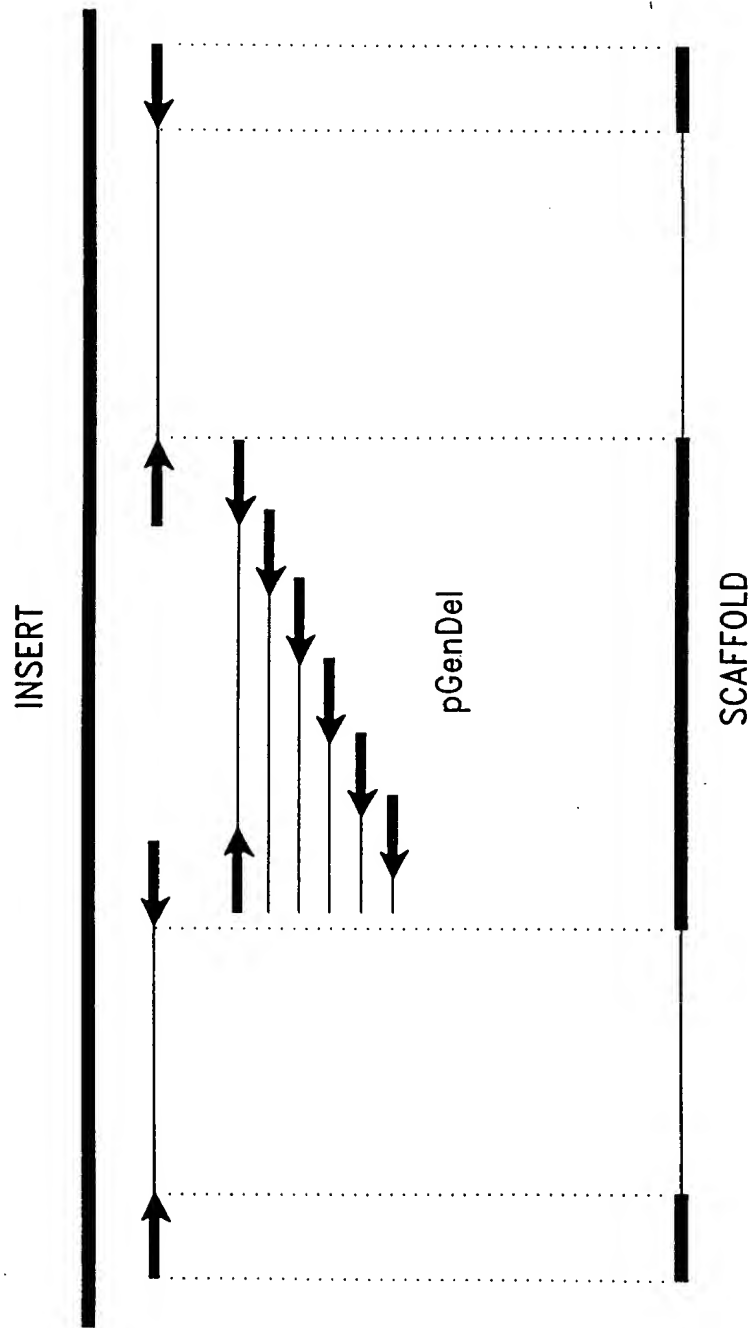


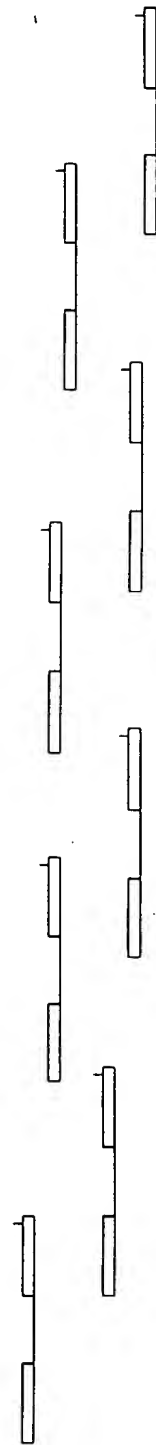
FIG.8





## B. ORDERED SHOTGUN SEQUENCING-OSS

1. SIMULTANEOUS SEQUENCING OF BOTH ENDS OF LIMITED NUMBER OF SUBCLONES(1.5-2 FOLD SEQUENCE COVERAGE).
2. ASSEMBLY OF MINIMAL TILING PATH OF SUBCLONES BY PAIRWISE SEQUENCE OVERLAP.
3. PRIMER WALKING FOR EXTENSIVE SEQUENCING OF MINIMAL TILING PATH SUBCLONES



**FIG.9B**



PAIRWISE ONLY	29023,2	45244,2	58801,3	68316,9	75206,4	79971,4	83504,1	85720,1	87923,1	88876,5	89630	90447,7	91191,6	91627,5	91925,6	92286,5	92591,5
MULTIPLE NUCLEATION	0	0	65553,8	83342,9	90466	93252,9	94234,1	94791,3	95127,1	95519,8	95770,1	96043,3	96178,7	96361,7	96443,5	96591,5	
POINT	0	50	150	200	250	300	350	400	450	500	550	600	650	700	750	800	

THE MAXIMUM SCAFFOLD LENGTH

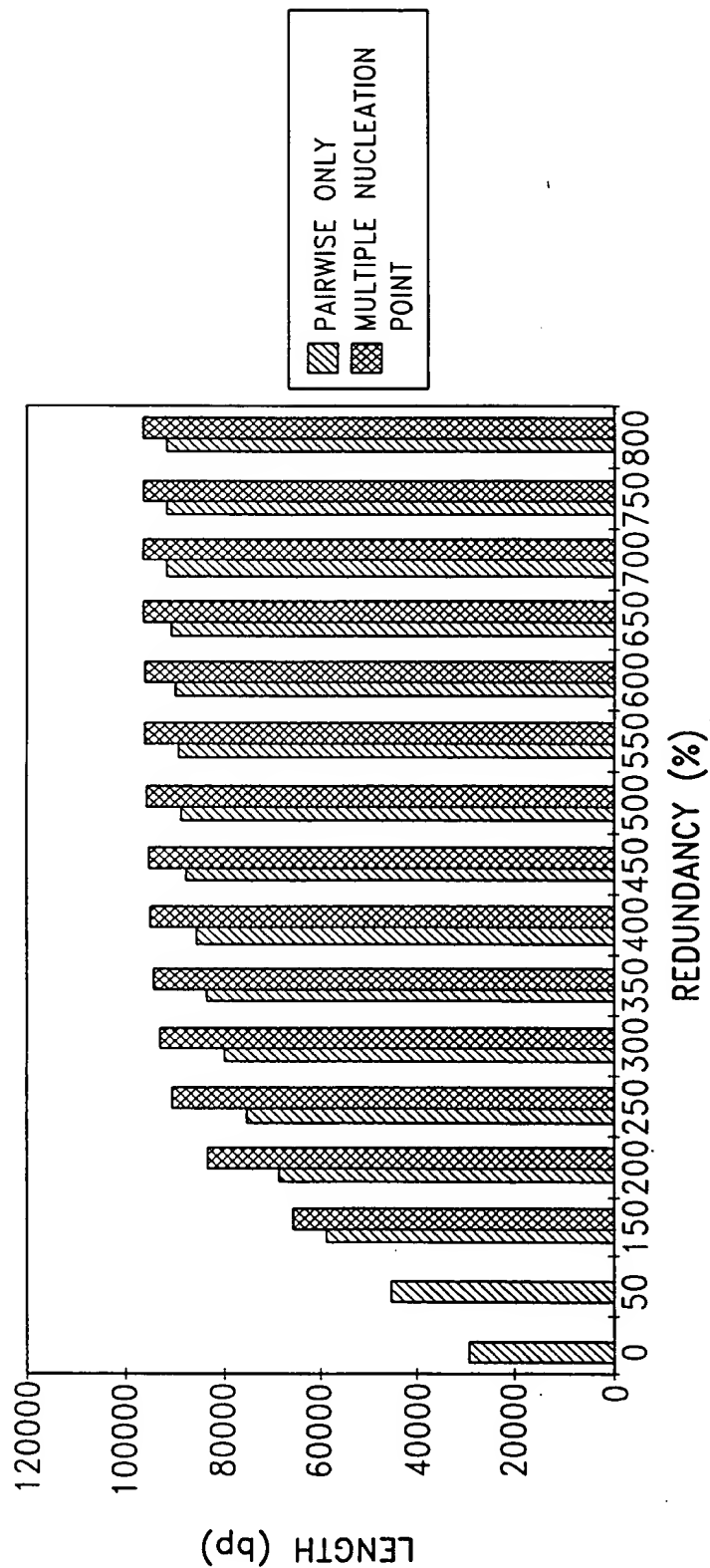
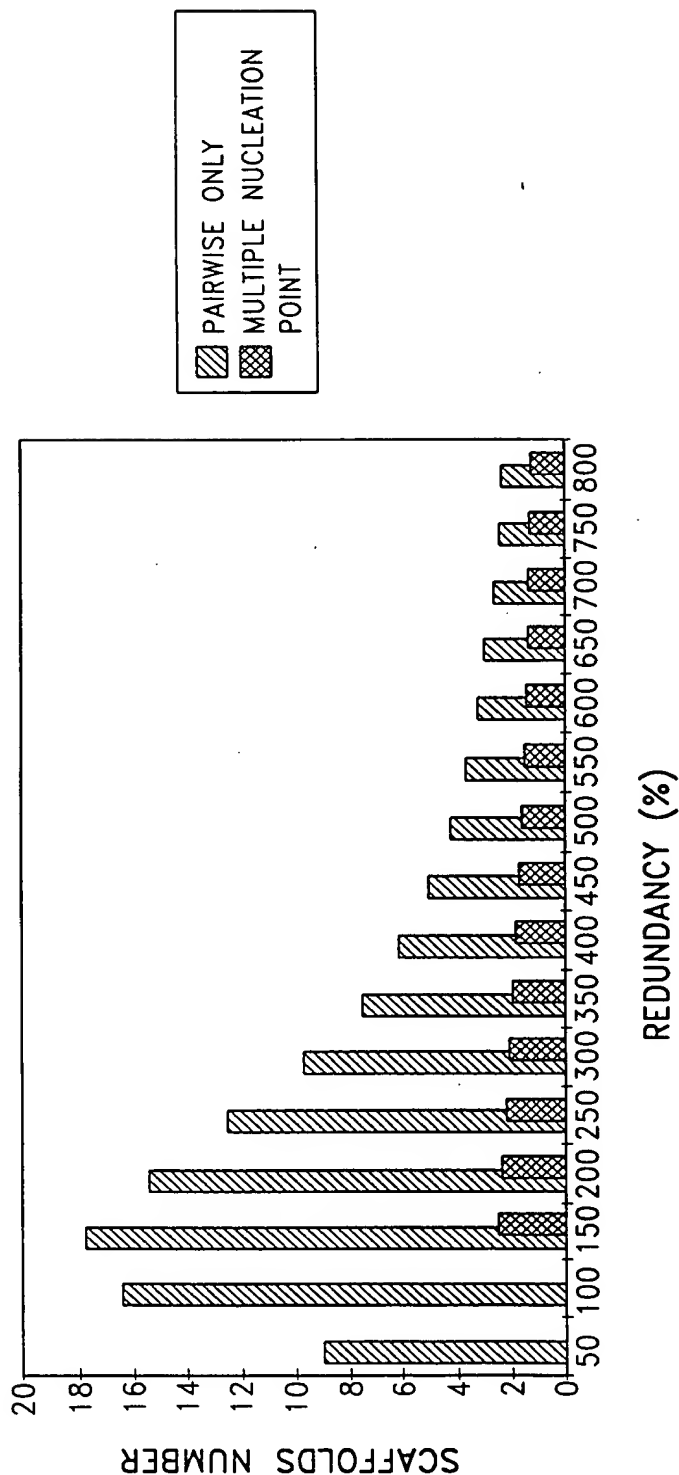


FIG. 10

PAIRWISE ONLY	8,908	16,455	17,729	15,476	2,338	2,185	9,701	7,522	6,11	4,974	1,676	4,208	3,662	1,484	550	600	650	700	750	800
MULTIPLE NUCLEATION	0	0	2,5	2,338	2,185	2,046	1,931	1,808	1,676	1,577	1,484	1,374	1,302	1,264	1,264	1,43	2,894	2,655	2,467	2,274
POINT																				

# THE SCAFFOLDS NUMBER



**FIG. 11**

PAIRWISE ONLY	2.02868	2.64877	3.13585	3.67497	3.77673	3.72902	3.33939	3.00032	2.60141	2.31273	2.12644	1.92935	1.76033	1.64194	1.53327	1.41807
MULTIPLE NUCLEATION	0	0	1.20333	1.59241	1.65915	1.63765	1.53826	1.42167	1.30039	1.16708	1.01968	0.94504	0.83793	0.78088	0.74216	0.66806

# STANDARD DEVIATION OF THE SCAFFOLDS NUMBER

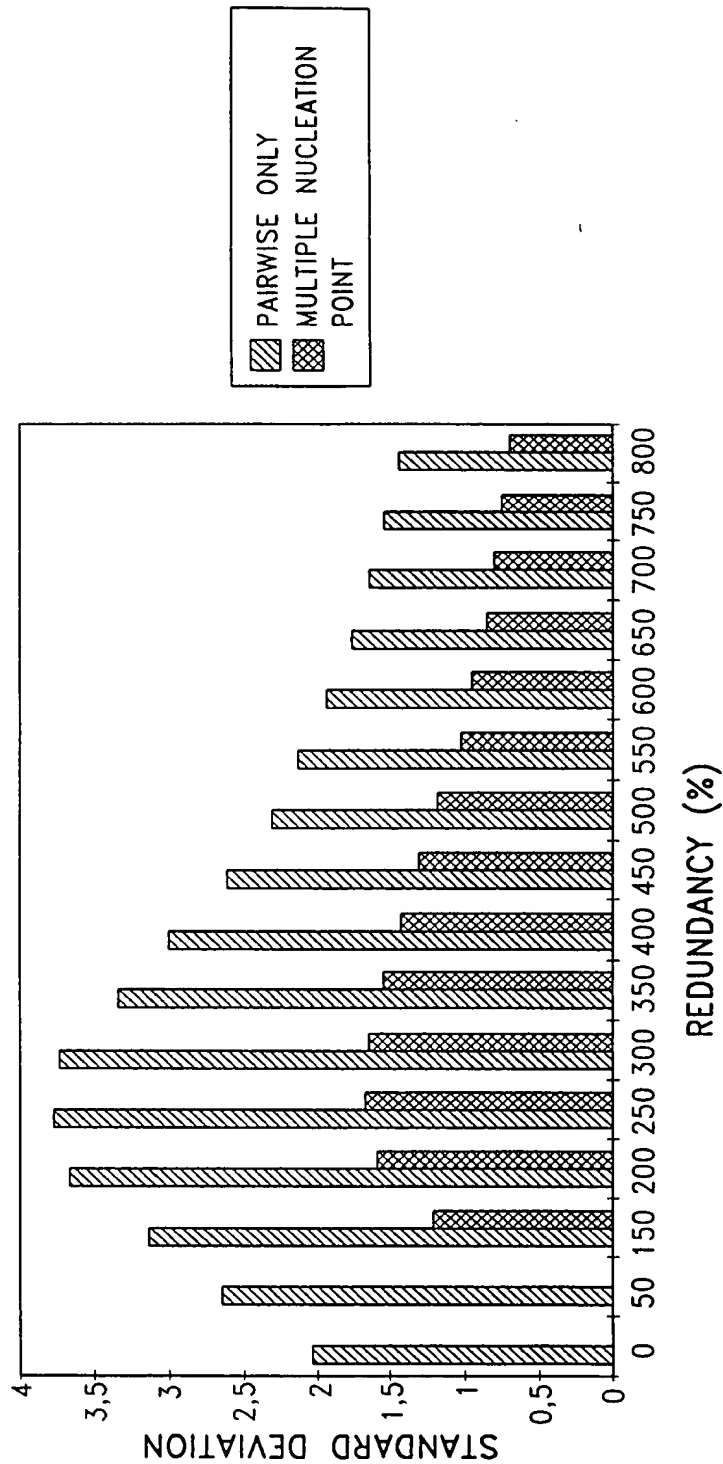
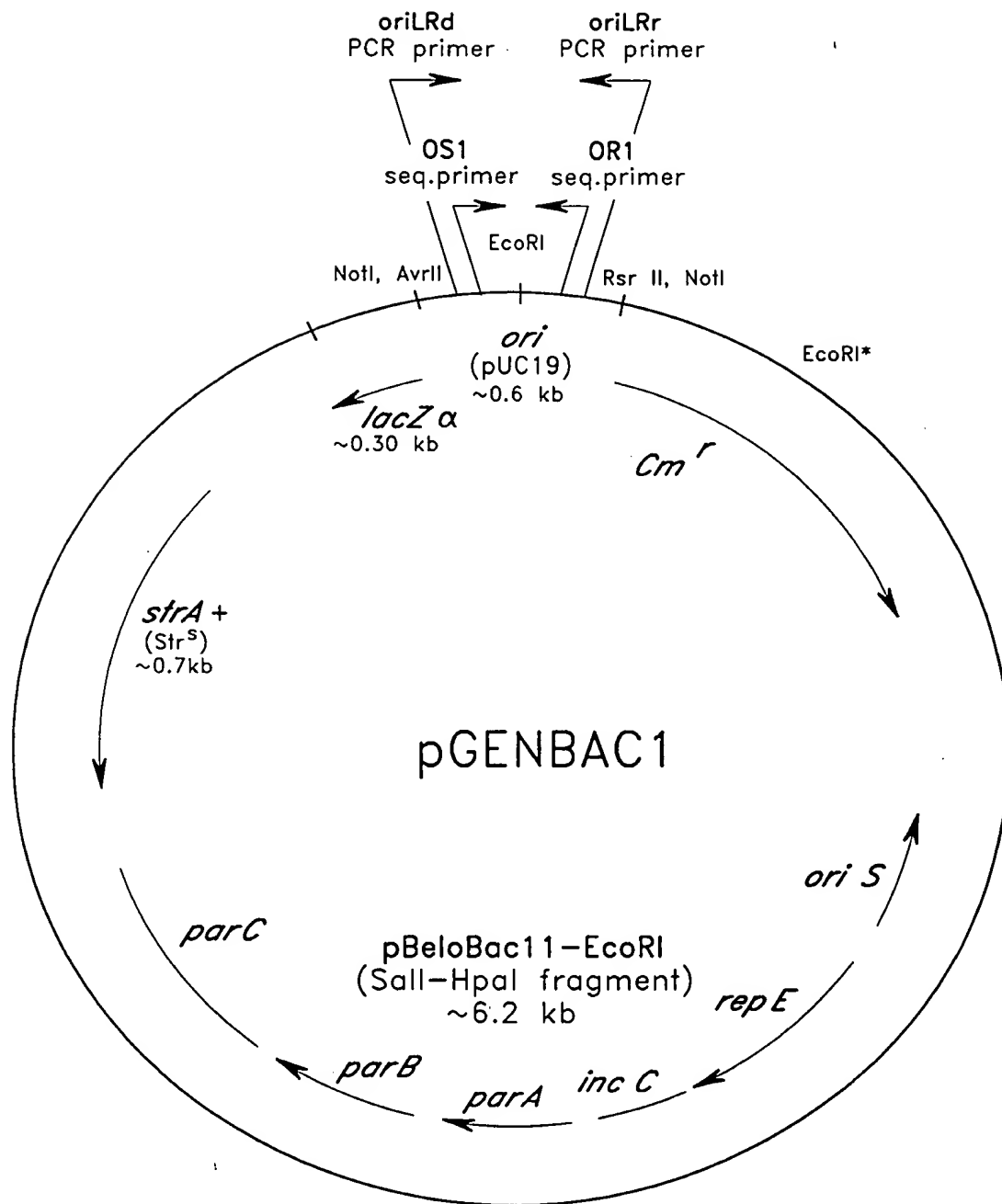
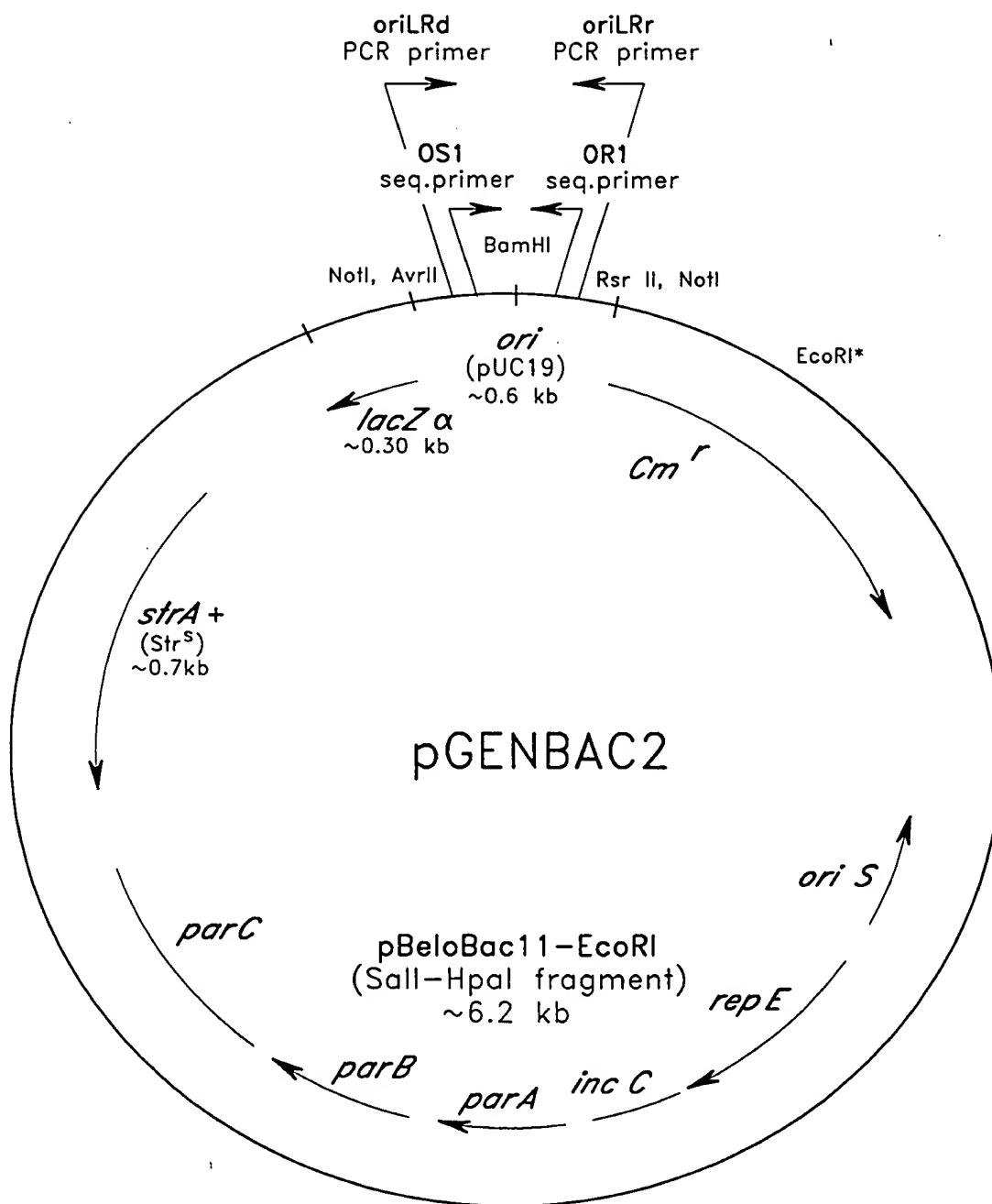


FIG.12



**FIG. 13**



**FIG. 14**